

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2002, 20:18:52 ; Search time 1839 Seconds
(without alignments)
3971.376 Million cell updates/sec

Title: US-09-728-446-819

Perfect score: 349
Sequence: 1 tatataatgaatacctgctg.....gnttgagcttggaagtttg 349

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match length DB ID Description

1	151.4	43.4	1328	10	BC004743	BC004743 Mus musculus
2	151.4	43.4	1345	10	MMU08039	U08039 Mus musculus
3	146.6	42.0	1292	10	MMU08990	U08990 Mus musculus
4	146.6	42.0	164796	10	AC083947	AC083947 Mus musculus
5	135.4	38.8	881	10	AF268469	AF268469 Rattus no
6	135.4	38.8	1380	10	AB039664	AB039664 Rattus no
7	133.2	38.2	879	4	AF268466	AF268466 Bos taurus
8	132.2	37.9	825	10	AF048829	AF048829 Rattus no
9	132.2	37.9	828	10	AF048830	AF048830 Rattus no
10	130.6	37.4	1077	9	HSU90943	U90943 Homo sapien
11	130.6	37.4	1209	6	AR017815	AR017815 Sequence
12	130.6	37.4	1364	9	AK058201	AK058201 Homo sapi
13	130.6	37.4	1393	6	AR103434	AR103434 Sequence
14	130.6	37.4	1851	9	BC002456	BC002456 Sus scrofa
15	127.4	36.5	879	4	AF268473	AF268473 Sus scrofa
16	122	35.0	879	4	AF268473	AF268473 Sus scrofa
17	121	34.7	163272	9	CNS01DUT	U08038 Mus musculus
18	82.2	23.6	237	4	BT299423	BT299423 Bos taurus
19	69.8	20.0	1317	10	BC003731	BC003731 Mus musculus
20	69.8	20.0	1662	10	MMU30838	U30838 Mus musculus
21	67.4	19.3	324	6	AX341725	AX341725 Sequence
22	67.4	19.3	848	9	HS3YDAC3	AF151681 Homo sapi
23	67.4	19.3	89921	2	AF170802	AF170802 Homo sapi
24	67.4	19.3	94060	2	AF216673	AF216673 Homo sapi
25	67.4	19.3	164419	2	AC104387	AC104387 Homo sapi
26	67.4	19.3	165041	2	AC107885	AC107885 Homo sapi
27	66.6	19.1	930	10	AF268468	AF268468 Rattus no
28	66.6	19.1	1715	10	AB039663	AB039663 Rattus no
29	65	18.6	885	4	BT288914	BT288914 Bos taurus
30	65	18.6	907	4	AF268462	AF268462 Sus scrofa
31	63.4	18.2	920	4	AF268465	AF268465 Bos taurus
32	63.4	18.2	1404	9	HUMVDAC2X	L06328 Human volta
33	63.4	18.2	1464	9	HUMVDAC2X	L06328 Human volta
34	63.4	18.2	1477	9	BC001283	BC001283 Homo sapien
35	63.4	18.2	1522	9	BC000165	BC000165 Homo sapi
36	59.6	17.1	130049	2	AC073296	AC073296 Mus musculus
37	59.6	17.1	154256	2	AC073295	AC073295 Mus musculus
38	59.6	17.1	238039	2	AL596103	AL596103 Mus musculus
39	57.4	16.4	647	10	AF441736	AF441736 Mus musculus
40	57.4	16.4	191750	2	AC024113	AC024113 Mus musculus
41	57	16.3	921	4	AF268472	AF268472 Oryctolagus
42	56.6	16.2	932	5	AF268474	AF268474 Gallus gallus
43	54.8	15.7	230384	2	MMU5XDNA	AL669964 Mus musculus
44	54.8	15.7	241432	10	AL589661	AL589661 Mouse DNA

ALIGNMENTS

RESULT 1	BC004743	1328 bp	mus musculus	linear	rod 12-jul-2001
LOCUS	BC004743				
DEFINITION	Mus musculus, voltage-dependent anion channel 3, clone MGC:5955				
ACCESSION	BC004743				
VERSION	BC004743.1	GI:13435770			
KEYWORDS	MGC.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Strausberg, R.				
TITLE	Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
JOURNAL	NIH-MGC Project URL: http://mgc.ncl.nih.gov				

REMARK
COMMENT
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE	JOURNAL	FEATURES SOURCE
1 (bases 1 to 1292)	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus.	1 (bases 1 to 1292)	Sampson, M.J., Lovell, R.S. and Craigen, W.J.	The murine voltage-dependent anion channel gene family. Conserved structure and function
J. Biol. Chem. 272 (30), 18966-18973 (1997)	9273603 9228078	2 (bases 1 to 1292)	Sampson, M.J., Lovell, R.S. and Craigen, W.J.	Direct Submission
		Submitted (19-FEB-1997)	College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Location/Qualifiers
		1..1292		/organism="Mus musculus"
		/db_xref="taxon:10090"		31..879
		/note="Processed pseudogene; similar to voltage dependent anion channel 3"		/codon_start=1
		/pseudo		
BASE COUNT	367 a 263 c 304 g 358 t			
ORIGIN				
Query Match	42.0%; Score 146.6; DB 10; Length 1292;			
Best Local Similarity	76.4%; Pred. No. 9,1e-35;			
Matches	201; Conservative 0; Mismatches 58; Indels 4; Gaps 3;			
OY 88	ATGGCGCTCGMACATATGGGCTCACCCTTACCACCAANANGAGATACAGCGGACTCTTGGG 147			
Db 217	AAGGCTCGACATATGGGCTCACCCTTACCACCAAGTGAATACAGACACCTTGGG 276			
OY 148	ACAGACCTTTTGTGAGAAATATGATGATGCTGAGGTTTAAACGTACTCTGATACCAT 207			
Db 277	ACAGAAATCTCTGGGAGAAATAG-TTGCGTGAAGCGTTGAACATGACTCTGATACCAT 335			
OY 208	ATTATACCATATGCTCCATATCTTTTATGTCATTTTCCGGCTCTATTCGCGCAT 267			
Db 336	ATTGTACCAACACAGGAA--AGAAAGTGTGGAATTAAGGCTCTATATGAGCGGAT 393			
OY 268	TGCTNNATTCGCGAGTATGTTGATNTNNATTTTTTGGACCGACCATCATATGAGT-G 326			
Db 394	TGTTTATGCTCGCGAGATATGTTTATATATTTTGTGAACGACCATATATGCTGG 453			
OY 327	TCTGNNTTGGCTTTGAAGTTG 349			
Db 454	GCTGTGTGGCTTTGAAGTTG 476			
RESULT 4				
AC083947	164796 bp DNA linear HTG 07-OCT-2000			
LOCUS	Mus musculus chromosome 13 clone RP33-25H6 strain C57BL6/J, WORKING			
DEFINITION	DRAFT SEQUENCE, 12 unordered pieces.			
AC083947	AC083947.1 GI:10716596			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 164796)			
	Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,			
	Bouffard, G.G., Dietrich, N.L., Gupta, J., Ho, S.-L., Idol, J.,			
	Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, O.L., Maduro, V.B.,			
	Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B.,			
	Stantilop, S., Thomas, J.W., Thomas, P.J., Tlonsong, E.E.,			
	Touman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A., Wetherby, K.D. and			
	Green, E.D.			
TITLE	NISC Mouse Sequencing Initiative			
JOURNAL	Unpublished			

```

REFERENCE      2 (bases 1 to 164796)
AUTHORS       Green,E.D.
TITLE         Direct Submission
JOURNAL       Submitted (07-OCT-2000) NIH Intramural Sequencing Center, 8717
              Government Circle, Gaithersburg, MD 20877, USA

COMMENT
-----
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mousehgri.nih.gov
Project Information
-----
Center project name: tw
Center clone name: 025H06
-----
Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159902 bases at least Q40
Consensus quality: 161129 bases at least Q30
Consensus quality: 161677 bases at least Q20
Insert size: 214000; agarose-fp
Insert size: 163696; sum-of-contigs
Quality coverage: 4.41x in Q20 bases; agarose-fp
Quality coverage: 5.76x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
*
* 1          3970: contig of 3970 bp in length
* 3971          4070: gap of unknown length
* 4071          10761: contig of 6691 bp in length
* 10762          10861: gap of unknown length
* 10862          17452: contig of 6591 bp in length
* 17453          17552: gap of unknown length
* 17553          26556: contig of 9104 bp in length
* 26557          26757: gap of unknown length
* 26757          36514: contig of 9758 bp in length
* 36515          36615: gap of unknown length
* 36615          48913: contig of 13199 bp in length
* 48913          49914: gap of unknown length
* 49914          60113: contig of 10200 bp in length
* 60114          60213: gap of unknown length
* 60214          73387: contig of 13173 bp in length
* 73387          73487: gap of unknown length
* 73487          91199: contig of 17713 bp in length
* 91200          91299: gap of unknown length
* 91300          115064: contig of 23765 bp in length
* 115065          115164: gap of unknown length
* 115165          139733: contig of 24569 bp in length
* 139734          139833: gap of unknown length
* 139834          164796: contig of 24963 bp in length.
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* Location/Qualifiers
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* 1..164796
*   organism="Mus musculus"
*   strain="C57BL6/J"
*   db_xref="taxon:10090"
*   chromosome="13"
*   clone="RP23-25H6"
*   /clone.lib="RPCI mouse BAC library 23"
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* 1..3970
*   note="assembly_fragment"
*   /note="assembly_fragment"
* 4071..10761
*   note="assembly_fragment"
* 10862..17452
*   note="assembly_fragment"
* 17553..26656
*   note="assembly_fragment"
* 26757..36514

```


Tel:81-886-33-7278, Fax:81-886-33-9512)

FEATURES
source
1. 1380
Location/Qualifiers/organism="Rattus norvegicus"
/db_xref="taxon:10116"gene
90..941
/gene="VDAC3"CDS
90..941
/gene="VDAC3"/codon_start=1
/product="mitochondrial voltage dependent anion channel"

/protein_id="BAB13475.1"

/db_xref="gi:10119782"

/translation="MCSTPTCDLGKAAKDVFNKGFGMWKIDLRKSCGSEST
GHAYDTGKASGNLETKYKICNVGLFTQKNMTDNTLTETISEMKLAEGKLTIDTI
FVPTNGKSKGLAKASYRDCFSVSGKVIDFSGPTIYGMAVLAFGMLAGYOMSPDTA
KSKLCONNFALGYKAEDPOLHTHVNDGTFEGSIYOKVNEK IETSIINLAWTGSNNT
FGIAKRYLDRTSLSAKVNNSLIGLGYTQSLRPGVKLTLSALVDGRFNAGHKV
LGFELEA"BASE COUNT 402 a 272 c 334 g 372 t
ORIGIN

Query Match 38.8%; Score 135.4; DB 10; Length 1380;

Best Local Similarity 73.8%; Pred. No. 2.8e-31;

Matches 194; Conservative 0; Mismatches 65; Indels 4; Gaps 3;

OY 88 ATGGGCTGCNACTATGGCGCTCATTACCCANANGAGTACNACGGTACTCTGGG 147

DB 276 AAGGCTGTACTACGGGCTCATCTTACCCAAAGTGAATACACACATCTCTGGG 335

OY 148 ACAGACCTTTTNGAGAAATGTCATGCTGANGGTTNAACTGCTGATACCAT 207

DB 336 ACAGAAATCTCTGGAGAAATAAG-TTGGCTGAAGGCTTGAACCTGAGGTTGATACCAT 394

OY 208 ATTATACCATNCNCTCCATCTTTAGTCCATTTCGCCGCTCTCTATGGCCGNAAT 267

DB 395 ATTTTACCACAAACACAGGGA--AGAAGAGTGGGAATTAAGGCTCTATGACGGGAT 452

OY 268 TGNTNNANTCTGGCAGTAATGTGATNNATTTTTCGACCGCCTCATATGGCT-G 326

DB 453 TCTTTAGTGTGGCAGTAAAGTTTCTTGACCGCCTCATATGGCTGG 512

OY 327 TCTGNNTTGGCCTTTGAAGTTG 349

DB 513 GCCGTGTGGCCTTTGAAGTTG 535

RESULT 7

AF268466 879 bp mRNA linear MAY 29-JUN-2000

LOCUS Bos taurus voltage-dependent anion channel 3 (VDAC3) mRNA, complete

ACCESSION AF268466
AF268466.1 GI:8810223

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source
1..879
/organism="Bos taurus"
/db_xref="taxon:9913"gene
1..879
/cell_type="lens fiber"
/gene="VDAC3"primer_bind
1..23
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Accession Number NK_005662"CDS
1..852
/gene="VDAC3"/codon_start=1
/product="voltage-dependent anion channel 3"

/protein_id="AAF80103.1"

/db_xref="gi:8810224"
/translation="MCNTPPTCDLGKAAKDVFNKGFGMWKIDLRKSCGSEST
GHAYDTGKASGNLETKYKICNVGLFTQKNMTDNTLTETISEMKLAEGKLTIDTI
FVPTNGKSKGLAKASYRDCFSVSGKVIDFSGPTIYGMAVLAFGMLAGYOMSPDTA
KSKLCONNFALGYKAEDPOLHTHVNDGTFEGSIYOKVNEK IETSIINLAWTGSNNT
FGIAKRYLDRTSLSAKVNNSLIGLGYTQSLRPGVKLTLSALVDGRFNAGHKV
LGFELEA"BASE COUNT 264 a 179 c 218 g 218 t
ORIGIN

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Best Local Similarity 73.1%; Pred. No. 1.3e-30;

Matches 193; Conservative 0; Mismatches 67; Indels 4; Gaps 3;

OY 87 CATGGCTGCNACTATGGCGCTCATTACCCANANGAGTACNACGGTACTCTGGG 146

DB 186 CAAGATCTGTAACTATGAGACTGACCTTACGACGAGTGAACACACACATCTCTGGG 245

OY 147 GACGACCTTTTNGAGAAATGTCATGCTGANGGTTNAACTGCTGATACCA 206

DB 246 GACGAAATCTCTGGAGAAATAAG-TTGGCTGAAGGTTGAACCTGCTTGAATACCA 304

OY 207 TATTNTACCATNCNCTCCATCTTTAGTCCATTTCGCCGCTCTCTATGGCCGNA 266

DB 305 TATTGTACCGAACAACAGAA--AGAAGAGTGGGAATTAAGGCTCTATTAACGGGA 362

OY 267 TGNTNNANTCTGGCAGTAATGTGATNNATTTTTCGACCGCCTCATATGGCT- 325

DB 363 TTGTTTACGCTTGGCAGTAATGTGATATAGATTTTTCGACCGCCTCATATGGCTG 422

OY 326 GTCTGNNTTGGCCTTTGAAGTTG 349

DB 423 GGCTGTGTGGCCTTTGAAGTTG 446

RESULT 8

AF048829 825 bp mRNA linear ROD 03-APR-1999

LOCUS Rattus norvegicus voltage dependent anion channel (RVDAC3) mRNA,

ACCESSION AF048829
AF048829.1 GI:4558731

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source
1..825
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/db_xref="taxon:10116"
/tissue_type="heart"
/gene="RVDAC3"

BASE COUNT		245 a	155 c	213 g	215 t
ORIGIN					
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Query Match	37.9%	Score 132.2;	DB 10;	Length 828;	
Best Local Similarity	73.0%	Pred. No. 2,76-30;			
Matches 192;	Conservative	0;	Mismatches 67;	Indels 4;	Gaps 3;
OY	88	ATGGCGTCGNCMTATGGGCTCACCTTCACCCANMNGNAGACAGACGACTCTTGGG	147		
DB	163	AAGGCTGTGAACCTACCGGCTCATCTTCCACCCAAAAGTGGATACGAGAAATCTTTGGG	222		
OY	148	ACAGACCTTTTGTGAGAAATNTGCATGCTGANGGGTTNNAACTGACTCGATATACCAT	207		
DB	223	ACAGAAATCTCTTTGGGAGAAATAG-TTGGCTGAAGGGTTGAACCTGACGGTTGTATACAT	281		
OY	208	ATTMTACCAATNCNCTCMTATCCTTTTGTGTCGCATTTTCCGGGCTCCTATTCGCNMAT	267		
DB	282	ATTTTACCAACACACAGGGA--AGAAAGTGTGGAAATTAAGGCTCTATAGACGGGAT	339		
OY	268	TGNTNNANTCTGGCAGATATGTTGATNTNNAATTTTTCTGGACGACCATATATGGCT-G	326		
DB	340	TGTTTAGTGCGCAGTAGAGTTGCATATGATTTTCTGTGACCGACCATCTATAGCGTGG	399		
OY	327	TCTGNNTTGGCCTTGAAGGTTG	349		
DB	400	GCGGTGTGGCTTTCGAAGGTTG	422		
RESULT	10				
LOCUS	HSU90943				
DEFINITION	Homo sapiens voltage dependent anion channel form 3 mRNA, complete cds.	1077 bp	mRNA	linear	PRI 23-OCT-2001
ACCESSION	U90943				
VERSION	U90943.1				
KEYWORDS	GI:2735306				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1077)				
AUTHORS	Rahmani,Z., Manouiry,C. and Siddiqui,A.				
TITLE	Isolation of a novel human voltage-dependent anion channel gene				
JOURNAL	Eur. J. Hum. Genet. 6 (4), 337-340 (1998)				
MEDLINE	98454325				
PUBMED	9781040				
REFERENCE	2 (bases 1 to 1077)				
AUTHORS	Rahmani,Z. and Siddiqui,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-FEB-1997) URA 1335 CNRS, Hopital Necker-Enfants Malades, 156 Rue de Vaugirard, Paris 75015, France				
FEATURES	location/Qualifiers				
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	1..852				
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	/db_xref="GI:2735307"				
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CDS					
BASE COUNT	310 a	207 c	264 g	296 t	
ORIGIN					

Query Match 37.4%; Score 130.6; DB 9; Length 1077;
 Best Local Similarity 72.6%; Pred. No. 8.7e-30;
 Matches 191; Conservative 0; Mismatches 68; Indels 4; Gaps 3;

QY 88 ATGGGCTGCNACTATGGCTCACCTTCACCCANANGNGAGTACNGAGCTACTCTGGG 147
 DB 187 AAGGTCTGTACTATGACTTACTTACCCAGAAATGAGAACACAGCACTACTCTAGG 246
 QY 148 ACAGACCTTTTNGAATNTGCATGCTGANGGTTNAACTGACTCTGCATACCAT 207
 DB 247 ACAGAAATCTCTGGAGATAAG-TTGGCTGAAGGGTTGAACCTGACTCTGTATACCAT 305
 QY 208 ATTNTACCATNCCTCCNATCCTTTAGTCCCTTTCCCGCCCTCTATTCGCNAT 267
 DB 306 ATTTGTACCGAACAGGAA--AGAGAGTGGGAAATTAAGGCTCTCTNAAAGGGGAT 363
 QY 268 TGTNNANTCTCGCAGTAATGTGATNTNATTTTCTGGACCGACCATCTATGCT-G 326
 DB 364 TGTTTTACTGTGGCAGTAATGTGATATGATTTTCTGGACCAACCATCTATGCTGG 423
 QY 327 TCTGNTTGGCCTTTGAAGGTTG 349
 DB 424 GCTGTGTGGCTTCGAAGGGTG 446

RESULT 11
 ARO17815 1209 bp DNA linear PAT 05-DEC-1998
 LOCUS ARO17815
 DEFINITION Sequence 2 from patent US 5780235.
 ACCESSION ARO17815
 VERSION ARO17815.1 GI:3973418
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1209)
 AUTHORS Bandman,O. and Hillman,J.L.
 TITLE Human voltage-dependent anion channel
 JOURNAL Patent: US 5780235-A 2 14-JUL-1998;
 FEATURES
 source Location/Qualifiers
 BASE COUNT 342 a 233 c 301 g 332 t 1 others
 ORIGIN

Query Match 37.4%; Score 130.6; DB 6; Length 1209;
 Best Local Similarity 72.6%; Pred. No. 8.7e-30;
 Matches 191; Conservative 0; Mismatches 68; Indels 4; Gaps 3;

QY 88 ATGGGCTGCNACTATGGCTCACCTTCACCCANANGNGAGTACNGAGCTACTCTGGG 147
 DB 280 AAGGTCTGTACTATGACTTACTTACCCAGAAATGAGAACACAGCACTACTCTAGG 339
 QY 148 ACAGACCTTTTNGAATNTGCATGCTGANGGTTNAACTGACTCTGCATACCAT 207
 DB 340 ACAGAAATCTCTGGAGATAAG-TTGGCTGAAGGGTTGAACCTGACTCTGTATACCAT 398
 QY 208 ATTNTACCATNCCTCCNATCCTTTAGTCCCTTTCCCGCCCTCTATTCGCNAT 267
 DB 399 ATTTGTACCGAACAGGAA--AGAGAGTGGGAAATTAAGGCTCTCTATTAAGCGGAT 456
 QY 268 TGTNNANTCTCGCAGTAATGTGATNTNATTTTCTGGACCGACCATCTATGCT-G 326
 DB 457 TGTTTTACTGTGGCAGTAATGTGATATGATTTTCTGGACCAACCATCTATGCTGG 516
 QY 327 TCTGNTTGGCCTTTGAAGGTTG 349
 DB 517 GCTGTGTGGCCTTCGAAGGGTG 539

RESULT 12
 AK058201 1364 bp mRNA linear PRI 31-OCT-2001
 LOCUS AK058201

DEFINITION Homo sapiens cDNA FLJ25472 fis, clone TST09616, highly similar to
 VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3.
 ACCESSION AK058201
 VERSION AK058201.1 GI:16554282
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens testis cDNA to mRNA, clone_11b:TST clone:TST09616.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
 Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
 Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
 Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
 Katsuka,R., Kuwa,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S.,
 Terashima,Y., Watanabe,M., Suzuki,Y., Hata,H., Nakagawa,K.,
 Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R.,
 Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B.,
 Nagai,K., Isogai,T. and Sugano,S.
 NEDO human cDNA sequencing project
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 1364)
 REFERENCE Sugano,S. and Suzuki,Y.
 AUTHORS Direct Submission
 JOURNAL Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure, Human Genome
 Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
 (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 FAX:81-3-5449-5416)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology (RAB); cDNA library
 construction and 5'-end one pass sequencing; Institute of Medical
 Science, University of Tokyo, Laboratory of Genome Structure, Human
 Genome Center; 3'-end one pass sequencing; RAB; clone selection for
 full insert sequencing; RAB and Helix Research Institute.
 FEATURES
 source Location/Qualifiers
 1. 1364
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 /clone="TST09616"
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 /clone_11b="TST"
 /note="cloning vector: pME18SPL3"
 BASE COUNT 383 a 266 c 330 g 385 t
 ORIGIN

Query Match 37.4%; Score 130.6; DB 9; Length 1364;
 Best Local Similarity 72.6%; Pred. No. 8.7e-30;
 Matches 191; Conservative 0; Mismatches 68; Indels 4; Gaps 3;

QY 88 ATGGGCTGCNACTATGGCTCACCTTCACCCANANGNGAGTACNGAGCTACTCTGGG 147
 DB 271 AAGGTCTGTACTATGACTTACTTACCCAGAAATGAGAACACAGCACTACTCTAGG 330
 QY 148 ACAGACCTTTTNGAATNTGCATGCTGANGGTTNAACTGACTCTGCATACCAT 207
 DB 331 ACAGAAATCTCTGGAGATAAG-TTGGCTGAAGGGTTGAACCTGACTCTGTATACCAT 389
 QY 208 ATTNTACCATNCCTCCNATCCTTTAGTCCCTTTCCCGCCCTCTATTCGCNAT 267
 DB 390 ATTTGTACCGAACAGGAA--AGAGAGTGGGAAATTAAGGCTCTCTATTAAGCGGAT 447
 QY 268 TGTNNANTCTCGCAGTAATGTGATNTNATTTTCTGGACCGACCATCTATGCT-G 326
 DB 448 TGTTTTACTGTGGCAGTAATGTGATATGATTTTCTGGACCAACCATCTATGCTGG 507
 QY 327 TCTGNTTGGCCTTTGAAGGTTG 349
 DB 508 GCTGTGTGGCCTTCGAAGGGTG 530

RESULT 13

AR103434
LOCUS AR103434 1393 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6087477.
ACCESSION AR103434
VERSION AR103434.1 GI:12815022
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Unpublished.
TITLE 1 (bases 1 to 1393)
Fajb.D.A. and Gimbirone,M.A. Jr.
JOURNAL Compositions and methods for the treatment and diagnosis of
cardiovascular disease
Patent: US 6087477-A 5 11-JUL-2000;
FEATURES
Location/Qualifiers
1..1393
BASE COUNT 406 a 269 c 333 g 385 t
ORIGIN
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Best Local Similarity 72.6%; Pred. No. 8.7e-30;
Matches 191; Conservative 0; Mismatches 68; Indels 4; Gaps 3;
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DB 276 AAGGCTGTAACTATGACTTACCTTCAACCCAGAAATGACACAGCAATATCTATAGG 335
QY 148 ACAGACCTTTTNGAGAAATNTGCATGCTGANGGTTNMAACTGACTCTGATACAT 207
DB 336 ACAGAAATCTCTGGAGAAATAG-TTGGCTGAAGGTTGAACACTGACTCTGATACAT 394
QY 208 ATTATACCATNCCTCCNATCTTTAGTGCATTTTCCGCTCTATTCGCGNAT 267
DB 395 ATTTACCGAAGACAGGAA--AGAAAGATGGGAATTTGAAGGCTCTATTAACGGGAT 452
QY 268 TGTNTNANTCTGGCAGTAAATGTTATNTTCTTGACGACCATCATGCTT 326
DB 453 TGTTTAGTGTGGCAGTAATGTTATATAGATTTTCTTGACCAACCATCTATG 766 512
QY 327 TCTGNTTGGCCTTTGAAGTTG 349
DB 513 GCTGTGTGGCTTCGAAGGTC 535
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BC002456 1851 bp mRNA linear PRI 12-JUL-2001
LOCUS Homo sapiens, voltage-dependent anion channel 3, clone MGC:1966
DEFINITION IMAGE:3343379, mRNA, complete cds.
ACCESSION BC002456
VERSION BC002456.1 GI:12803280
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgtl.nih.gov
Shewchenko,Y., Welthery,K.D., Beckstrom-Sternberg,S.M., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Dietrich,N.L.,
Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Statliper,S., Thomas,P.J.,
Tlonson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://imgc.llnl.gov>
Series: IRAL Plate: 5 Row: h Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 3329393.
FEATURES
Location/Qualifiers
1..1851
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AKSLSONNFALGFKADPOLHTVNDTEFGSGIYOKVNEKETISINLAWTGSNNT
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BASE COUNT 541 a 388 c 435 g 487 t
ORIGIN
Query Match 37.4%; Score 130.6; DB 9; Length 1851;
Best Local Similarity 72.6%; Pred. No. 8.7e-30;
Matches 191; Conservative 0; Mismatches 68; Indels 4; Gaps 3;
QY 88 ATGGCTGCMCTATGGGCTCACCTTCAACCCANANGAGAGTACGAGGTACTCTGGG 147
DB 270 AAGGCTGTAACTATGACTTACCTTCAACCCAGAAATGACACAGCAATATCTATAGG 329
QY 148 ACAGACCTTTTNGAGAAATNTGCATGCTGANGGTTNMAACTGACTCTGATACAT 207
DB 330 ACAGAAATCTCTGGAGAAATAG-TTGGCTGAAGGTTGAACACTGACTCTGATACAT 388
QY 208 ATTATACCATNCCTCCNATCTTTAGTGCATTTTCCGCTCTATTCGCGNAT 267
DB 389 ATTTACCGAAGACAGGAA--AGAAAGATGGGAATTTGAAGGCTCTATTAACGGGAT 446
QY 268 TGTNTNANTCTGGCAGTAAATGTTATNTTCTTGACGACCATCATGCTT 326
DB 447 TGTTTAGTGTGGCAGTAATGTTATATAGATTTTCTTGACCAACCATCATGAGGTC 506
QY 327 TCTGNTTGGCCTTTGAAGTTG 349
DB 507 GCTGTGTGGCTTCGAAGGTC 529
RESULT 15
AF209727 879 bp mRNA linear MAM 03-JAN-2000
LOCUS Oryctolagus cuniculus voltage-dependent anion channel 3 (VMA3)
DEFINITION AF209727
ACCESSION AF209727
VERSION AF209727.1 GI:6653664
KEYWORDS
SOURCE rabbit.

ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 879)
AUTHORS Rae, J. L.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1999) Physiology and Biophysics, Mayo Foundation,
200 1st Street SW, Rochester, MN 55905, USA
Location/Qualifiers
FEATURES
source 1. 879
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/strain="New Zealand White"
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ORIGIN
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Best Local Similarity 71.9%; Pred. No. 8.5e-29;
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QY 88 ATGGGCTGCNACTATGGCTGACCTTCAACCCANANGAGTAGTCNAGAGTACTCTGGG 147
Db 187 AAGGTCTGTAACATGAGCTACCTTCAACCCAGAAATGGAACACAGACACTCTGGGG 246
QY 148 ACAGACCTTTTGTGNGAATNTGATGCTGANGGGTTNAACCTGACTCGATACCAT 207
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QY 208 ATTNTACCATNCCTCCNATCTTTAGTGCATTTTCCGGGCTCTATTGCCMGAT 267
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QY 268 TGTNNANTCTGGCAGTATGTTGATNTNNATTTTCTTGACCGACATCTATGGCT-G 326
Db 364 TGTTTAGTCTTGAGAAATAGTTTGTGATATGATTCTTGACCAACCATCTATGGCTGG 423
QY 327 TCTGNNTTGGCTTTGAAGGTTG 349
Db 424 GCTGTGTGGCTTTGAAGGTTG 446

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